

Sequence Range: 1 to 5864

```
>BgIII
10 20 30 40 50 60 70 80 90 100
GACGGATCGGAGATCTCCGATCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATCGCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGT
CTGCCTAGCCCTCTAGAGGGGTAGGGGATACCAGCTGAGAGTCTGTTAGACGAGACTACGCGGTATCAATTTCGGTCAATAGACGAGGAGCAACACACAA

>MfeI
110 120 130 140 150 160 170 180 190 200
GGAGGTCTGAGTAGTCTCCGAGCAAAATTTAAGCTACAACAAGGCTTGACCGCAATTCATGAAGAATCTGCTTAGGGTTAGGCGTTTTCGG
CCTCCAGCGACTCATACGCGCTGCTTTTAAATTCGATGTGTTCGTTCCGAACTGGCTGTTAACGTACTTCTTAGACGAATCCCAATCCGCAAAACGC

>SpeI
210 220 230 240 250 260 270 280 290 300
CTGCTTCGCGATGTAGCGGCAGATATACGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCAATTAGTTCATAGCCCATATA
GACGAAGCGCTACATCCCGGCTATATATGCGCACTGTAACCTAATAACTGATCAATAATTATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATAT

>CMV_promoter
310 320 330 340 350 360 370 380 390 400
TGGAGTTCGCGGTACATAACTTACGGTAAATGGCCCGCTGCGTACCGCCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGT
ACCTCAAGCGCAATGTATTGAATGCCATTACCGGGCGGACCGACTGGCGGGTTCGTTGGGGCGGGTAATGCAGTTATTACTGCATACAAGGGTATCA

>NdeI
410 420 430 440 450 460 470 480 490 500
AACGCCAATAGGGACTTTCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCCACTTGGCAGTACATCAAGTGTATCATATGCGCAAGTACGCCC
TTGCGGTATTCCTGAAAGGTAACTGCAGTTACCCACCTGATAAATGCCATTTGACGGGTGAACCGTCATGTAGTTACATAGTATACGGTTCATCGCGG

>SnaBI
510 520 530 540 550 560 570 580 590 600
CCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCA
GGATAACTGCAGTTACTGCCATTACCGGGCGGACCGCTAATACGGGTCACTGTACTGGAATACCCCTGAAAGGTGAACCGTCACTGATGATGCAATACTAGT

610 620 630 640 650 660 670 680 690 700
TCGCTATTACCATGGTGTGCGGTTTGGCAGTACATCAATGGCGTGGATAGCGGTTTGACTACCGGGGATTTCAGTCTCCACCCCATTCAGCTCAA
AGCGATAATGGTACCTACGCCAAACCGCTCATGTAGTTACCGCACCTATCGCCAAACTGAGTGCCTTAAAGGTTACAGGTTGGGTAACCTGACGTT

710 720 730 740 750 760 770 780 790 800
TGGGAGTTTGTGTTGGCACCAAAATCAACGGGACTTTCAGAAATGTCGTAACAACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAG
ACCTCTAAACAAACCGTGGTTTGTAGTTCGCCCTGAAAGGTTTACAGCATTTGTTGAGGCGGGSTAACGCGTTTACCCGCATCCGCACATGCCACCCCTC

>SacI
810 820 830 840 850 860 870 880 890 900
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CAGATATATCTGCTCTCGAGAGACCGATTGATCTCTTGGGTGACGAATGACCGAATAGCTTTAATTATGCTGAGTGATATCCCTCTGGGTTCGACGATCA

>Ecl136II
>T7_promoter
910 920 930 940 950 960 970 980 990 1000
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ATTCGAACGGCGGTGGTTACCTTAACCTGAACCTAGAATAAAATCAACGACGACGATGATCTCAAGTAAGAAGATTTTTGGTCCACCGGGCGGCTCTCG
M D W T W I L F L V A A T R V H S >
SIGEY > S K K P G G P G K S >
910 920 930 903 TO 1335 OF A. PCV/HB. SIGEY-WNVCHU_0 980 990 1000>
10 20 30 4.5 TO 437 OF SIGEY-WNVCHU* 70 80 90 100>
10 1 1 TO 54 OF SIGEY 40 50>

>HindIII
>Kozak_sequence
>HindIII_linker_{Split}
1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
CGCGCCGTGAACATGCTGAAGCGCGGCATGCCCGCGTCTGAGCCTGATTGGCCTGAAGCGCGGCATGCTGAGCCTGATCGACGGCAAGGGCCCCATAC
GCGCGGCCTTGTACGACTTCGCGCGGTACGCGGCGCAGGACTCGGACTAACCGGACTTCGCGCGGTACGACTCGGACTAGCTGCGGTTCGCGGGTATG
R A V N M L K R G M P R V L S L I G L K R A M L S L I D G K G P I >
WNVCHU*
1010 1020 1030 903 TO 1335 OF A. PCV/HB. SIGEY-WNVCHU_70 1080 1090 1100>
110 120 130 1.5 TO 437 OF SIGEY-WNVCHU* 170 180 190 200>

>SfiI
1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
GCTTCGTCGCTGGCGCTTCTTCCGCTTCAACCGCATTCGCCCCACCGCGCGGTGCTGGACCGCTGGCGCGCGGTGAACAGCAGACCGCAT
CGAAGCAGACCGGGGACCGGAAGGAAGCGGAGTGGCGGTAACCGGGGTGGCGCGGCAAGCAGCTGGGACCGCGCGGCACTTGTTCGCTGCGCGTA
R F V L A L L A F P R F T A I A P T R A V L D R W R G V N K Q T A M >

>ApaI
>Bsp120I
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FIG 7

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4510      4520      4530      4540      4550      4560      4570      4580      4590      4600
GTGCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGGCTACACTAGAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG
CAGCATGTCTCAAGAACTTCACCACCGGATGTATGCCGATGTATCTCTCTGTCAATAACCATAGACGGGAGACGACTTCGGTCAATGGAAAGCCTTTTTC

4610      4620      4630      4640      4650      4660      4670      4680      4690      4700
AGTTGGTAGCTCTTGTATCCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAA
TCAACCATCGAGAACTAGGCCGTTTGTGTTGGTGGCGACCATCGCCACAAAAAACAACGTTCTGTCGTCTAATGCGCGCTTTTTTTCTAGAGTCTT

4710      4720      4730      4740      4750      4760      4770      4780      4790      4800
GATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGA
CTAGGAAACTAGAAAAAGATGCCCCAGACTGCGAGTCACTTGTCTTTGAGTGCAATTCCCTAAAACCACTACTCTAATAGTTTTTCTAGAGTGGATCT

4810      4820      4830      4840      4850      4860      4870      4880      4890      4900
TCTTTTAAATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGAGGCACCTATCTC
AGGAAAAATTTAATTTTACTTCAAAAATTTAGTTAGATTTCATATATACTCATTTGAACCAGACTGTCAATGGTTACGAAATAGTCACTCCGTGGATAGAG

>AhdI
4910      4920      4930      4940      4950      4960      4970      4980      4990      5000
AGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCTGACTCCCGCTCGTGTAGATAAATACGATACGGGAGGGCTTACCATCTCGCCCCAGTGTCTCAATG
TCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCATCTATTGATGCTATGCCCTCCCGAATGGTAGACGGGGTCACGACGTTAC

5010      5020      5030      5040      5050      5060      5070      5080      5090      5100
ATACCGGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGGAAGGGCCGAGCCAGAAAGTGGTCTTGCACCTTTATCCGCT
TATGGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTGGTGGCGCTTCCCGGCTCGCGCTCTCACAGGACGTTGAAATAGGCGGA

5110      5120      5130      5140      5150      5160      5170      5180      5190      5200
CCATCCAGTCTATTAAATTGTTGCCGGGAAGCTAGAGTAAAGTAGTTCGCCAGTTAATAGTTTTCGCAACGTTTGTGCAATTTGCTACAGGCATCGTGGTGC
GGTAGGTCAGATAAATAACACGCGCCTTCGATCTCAATTCATCAAGCGGTCAATTATCAAAACGCTTGCAACACGGTAACGATGTCCGTAGACCCACAG

5210      5220      5230      5240      5250      5260      5270      5280      5290      5300
ACGTCCTCGTTGGTATGGCTTCACTACGCTCCCGTTCCCAACGATCAAGGGGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTC
TCCGAGCAGCAAAACCATACCGAAGTAAGTCGAGGCCAAGGGTTGTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTCGCCAATCGAGGAAG

>PvuI
5310      5320      5330      5340      5350      5360      5370      5380      5390      5400
GGTCCTCCGATCGTTGTGAGAAAGTAAGTTGGCCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAATCTCTTACTGTCTATGCCATCCGTAAAGAT
CCAGGAGGCTAGCAACAGTCTTCAATTCAACCGCGTCACAATAGTGAGTACCAATACCGTCTGTACGTATTAAAGAAATGACAGTACGGTAGGCATTCTA

>ScaI
5410      5420      5430      5440      5450      5460      5470      5480      5490      5500
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CGAAAAGACACTGACCATCATGAGTTGGTTTCACTAAGACTTTATCACAATACGCGCTGGCTCAACGAGAACGGGCGCAGTTATGCCCTATTATGGCG

5510      5520      5530      5540      5550      5560      5570      5580      5590      5600
GCCACATAGCAGAACTTTAAAGTGCTCATCATGGAAGACGTTCTCGGGGCGAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCTGATGTAA
CGGTGTATCGTCTTGAATTTTACAGAGTAGTAACCTTTTGAAGAAGCCCGCTTTTGAGAGTTCTTAGAATGGCGACAACCTTAGGTCAAGCTACATT

5610      5620      5630      5640      5650      5660      5670      5680      5690      5700
CCCACTCGTGACCCCACTGATCTTCAGCATCTTTTACTTTTCAACAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAA
GGGTGAGCACGTGGGTGACTAGAAAGTCTAGAAATGAAAGTGGTCGCAAGACCCACTCGTTTGTGCTTCCGTTTACGGCGTTTTTCCCTTATT

>SapI
5710      5720      5730      5740      5750      5760      5770      5780      5790      5800
GGGCGACACGGAAATGTTGAATACTCATACTCTTCTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGACGGGATACATATTTGAATG
CCGCTGTGCTTTTACAACCTTATGATATGAGAAAGAAAGTTATAATACTTCTGTAATAGTCCCAATAACAGAGTACTCGCTATGTATAAACTTAC

5810      5820      5830      5840      5850      5860
TATTAGAAAAATAAACAAATAGGGGTTCGCGCACATTTCCCGCAAAAGTGCCACTGACGTC
ATAAACTTTTTTATTGTTTATCCCAAGGCGGTGTAAAGGGCTTTTACAGGTGGACTGCAG

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WMVCHU*
1110 1120 1130 903 TO 1335 OF A.PCV/HB.SIGBY-WMVCHU_70 1180 1190 1200
210 220 230 25 TO 437 OF SIGBY-WMVCHU* 270 280 290 300
1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
GAAGCACCTGCTGAGCTTCAAGAGGAGCTGGGACCCCTGACCAAGCCATCAACCGCCGACGAGCAAGCAAGAGCGCGCGGCAAGACCGGATTT
CTTCGTGGAGACTCGAAGTCTCTCGACCCGTGGGACTGGTCCGGTAGTTGGCGGCTGCTGCTGCTTCTTCGCGCGCCGCTTCTGGCGGTAA
K H L L S F K K E L G T L T S A I N R R S S K Q K K R G G K T G I
WMVCHU*
1210 1220 1230 903 TO 1335 OF A.PCV/HB.SIGBY-WMVCHU_70 1280 1290 1300
310 320 330 35 TO 437 OF SIGBY-WMVCHU* 370 380 390 400
>BstEII
>PaeR7I
>NotI >XhoI >BstBI
>NotI_introduction_[Split] >V5_epitope
1310 1320 1330 1340 1350 1360 1370 1380 1390 1400
GCGGTGATGATTGGCTGATCGCCAGCGTGGGCGCGCGCTCGAGGTCAACCCATCGAAGGTAAAGCCTATCCCTAACCCCTCTCTCGGCTCGATTCTA
CGGCACTACTAACCGGACTAGCGGTGCGACCCGCGCGCGGAGCTCCAGTGGTAAAGCTTCCATTCCGATAGGGATTGGGAGAGGAGCCAGAGCTAAGAT
A V M I G L I A S V G A
WMVCHU*
903 TO 1335 OF A.PCV/HB.SIGBY
5 TO 437 OF SIGBY-WMVCHU*
>AgeI >PmeI
>Polyhistidine_tag >BGH_polyadenylation_signal
1410 1420 1430 1440 1450 1460 1470 1480 1490 1500
CGCGTACCGGTATCATCATCAACCATCAACATTGAGTTTAAACCCGCTGATCAGCCCTGACTGTGCTTCTAGTTGCCAGCCATCTGTGTTTCCGCTTCCCT
GCGCATGCGCAGTAGTAGTGGTAGTGAATCAAAATTTGGGCGACTAGTCCGAGCTGACACGGAAGATCAACGGTCCGTAGACAACAACGGGAGGGG
1510 1520 1530 1540 1550 1560 1570 1580 1590 1600
CGTGCTTCCCTTGAACCTGGAAGGTGCGCACTCCCACTGTCTTCTTAATAAATGAGGAAATTCGATCGCATGTCTGAGTAGGTGCTATTCTATTCTG
GCACGGAAGGAACCTGGGACCTCCACGGTGAAGGGTGACAGGAAGGATTATTTTACTCCTTTAACGTAGCGTAACAGACTCATCCAGTAAGATAAGAC
>BbsI
1610 1620 1630 1640 1650 1660 1670 1680 1690 1700
GGGGGTGGGGTGGGCGAGGACAGCAAGGGGAGGATTGGGAAGACAAATAGCAGGCATGCTGGGATGCGGTGGCTCTATGGCTTCTGAGGCGGAAAGAA
CCCCACCCACCCCGCTCTGTCGTTCCTCCCTTCTTAACCTTCTGTTATCTGCTGCTAGCAGCCCTACGCCACCCGAGATACCGAAGACTCCGCTTCTTT
1710 1720 1730 1740 1750 1760 1770 1780 1790 1800
CCAGCTGGGGCTCTAGGGGGTATCCCCACGCGCCCTGTAGCGGCGCAATTAAGCGCGCGGGTGTGGTGTACGCGCAGCGTACCGCTACACTTCCAG
GGTGCACCCCGAGATCCCCATAGGGGTGCGGGGACATCGCCGCGTAATTCGCGCGCCACACCAATGCGCGCTGCACTGGCGATGTGAACGGTC
1810 1820 1830 1840 1850 1860 1870 1880 1890 1900
CGCCCTTACGCGCCGCTTCTTCCCTTCTTCTTCCCTTCTTCTGCGCAGCTTCGCGCGCTTCCCGCTCAAGCTTAAATCGGGGATCCCTTTAGGGTTC
CGGGATCGCGGGCGAGGAAAGCGAAGAGGGAAGGAAAGAGCGGTGCAAGCGGCGAAGGGGCGAGTTCGAGATTATGCCCGCTAGGGAATCCCAAG
>DraIII
1910 1920 1930 1940 1950 1960 1970 1980 1990 2000
CGATTATTAGTCTTTACGGCACCTCGACCCCAAAAACTTGAATTAGGTGATGGTTACAGTGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGA
GCTAAATCAGAAATCCGCTGAGCTGGGTTTTTTGAATTAATCCACTACCAAGTGCAATCACCCGCTAGCGGGACTATCTGCCAAAAAGCGGGAACCT
2010 2020 2030 2040 2050 2060 2070 2080 2090 2100
CGTTGGAGTCCACGTTCTTAAATAGTGGACTCTTGTTCCTAACTGGAACAACTCAACCTATCTCGGTCTATTCTTTTGAATTATAAGGATTTTGGG
GCAACCTCAGGTGCAAGAAATATCACTGAGAACAAAGTTTGACCTTGTGTGAGTTGGGATAGAGCCAGATAAGAAAACTAAATATTCCCTAAAGCCC
2110 2120 2130 2140 2150 2160 2170 2180 2190 2200
GATTCGCGCTTATTGTTTAAAAATGAGCTGATTTAAACAAAAATTTAACGCGAATTAAATCTGTGGAATGTGTGTCAGTTAGGGGTGTGGAAGTCCCGAG
CTAAAGCCGGATACCAATTTTACTCGACTAAATTTGTTTTAAATTTGGGCTTAAATTAAGACACCTTACACACAGTCAATCCACACCTTTCAGGGGTC
2210 2220 2230 2240 2250 2260 2270 2280 2290 2300
GCTCCCCAGGCGGCAAGATATGCAAGCATGCACTCAATTAGTCAGCAACCGAGGTGTGGAAGTCCCGAGGCTCCCGAGCGAGCAAGATATGCAAA
CGAGGGGTCCGCTCTCTACAGCTTTCGTACGTAGAGTTAATCAGTCGTGTGTCACACCTTTTCAGGGGTCCGAGGGGTGCTCCGCTTTCATACGTTT
2310 2320 2330 2340 2350 2360 2370 2380 2390 2400
GCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTAACTCCGCCCATTCCTCCGCCCATGGCTG
CGTACGTAGATTAAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGTCAAGGCGGGTAAGAGGCGGGTACCAGAC
>AvrII
>StuI
2410 2420 2430 2440 2450 2460 2470 2480 2490 2500
ACTAATTTTTTTTATTTATGAGAGGCGGAGGCGGCTCTGCTCTGAGCTATTCCAGAAAGTAGTGAGGAGGCTTTTTTGGAGGCTTAGGCTTTTGCAAA
TGATTAATAAAATAATACGTCTCCGGCTCCGGCGGAGACGAGAGCTCGATAAGGTCTTCATCACTCTCCGAAAAAACCTCCGGATCCGAAAAACGTTT
>SmaI
>XmaI >BsaBI
2510 2520 2530 2540 2550 2560 2570 2580 2590 2600
AAGCTCCCGGAGCTTTGATATCCATTTCGGATCTGATCAAGAGACAGGATGAGGATCGTTTCGCAATGATTGAACAGATGGATTGCAACGAGGTTCCT
TTGAGGGCCCTCGAACAATATAGGTAAGAGCCTAGACTAGTTCTCTGCTCTACTCTAGCAAGCGTACTAACTTGTCTACTTAACGTGCGTCCAAGAG